



SEQUENCE LISTING

<110> AMRAD Operations Pty Ltd

<120> A NOVEL MAMMALIAN GENE, bcl-2, BELONGS TO THE bcl-2  
FAMILY OF APOPTOSIS-CONTROLLING GENES

<130> 2096584

<140> 09/155,327

<141> 1997-03-27

<150> PN8965

<151> 1996-03-27

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 33

<212> DNA

<213> Mouse

<220>

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33

<210> 2

<211> 9

<212> PRT

<213> Mouse

<220>

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<223> Xaa is Ile or Val

<400> 2

Asn Trp Gly Arg Xaa Val Ala Phe Phe

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5

<210> 3

<211> 31

<212> DNA

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<222> 4

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Trp Ile Gln Xaa Xaa Gly Gly Trp

1

5

<210> 5

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<400> 5

Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val

1

5

10

<210> 6  
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<220>  
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 <222> (1)..(579)

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ttt gta ggt tat aag ctg agg cag aag ggt tat gtc tgt gga gct ggc	96
Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
gta gcc ttc ttt gtc ttt ggg gct gca ctg tgt gct gag agt gtc aac	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala	
115 120 125	

tac ctg gag acg cgg ctg gct gac tgg atc cac agc agt ggg ggc tgg 432  
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
 130 135 140

gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg 480  
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
 145 150 155 160

cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg 528  
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
 165 170 175

gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576  
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 Lys

<210> 7  
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 <213> HUMAN

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 35 40 45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
 50 55 60

Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
 65 70 75 80

Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
85 90 95

Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
100 105 110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala  
115 120 125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
130 135 140

Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
145 150 155 160

Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
165 170 175

Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
180 185 190

Lys

<210> 8

<211> 582

<212> DNA

<213> Mouse

<220>

<221> CDS

<222> (1)..(579)

<400> 8

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Met Ala Thr Pro Ala Ser Thr Pro Asp Thr Arg Ala Leu Val Ala Asp  
1 5 10 15

ttt gta ggc tat agg ctg agg cag aag ggt tat gtc tgt gga gct ggc	96
Phe Val Gly Tyr Arg Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly	
20 25 30	
cct ggg gaa ggc cca gcc gcc gac ccg ctg cac caa gcc atg cgg gct	144
Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala	
35 40 45	
gct gga gac gag ttt gag acc cgt ttc cgc cgc acc ttc tct gac ctg	192
Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
50 55 60	
gcc gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
65 70 75 80	
cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
aaa gaa atg gag cct ttg gtg gga caa gtg cag gat tgg atg gtg gcc	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala	
115 120 125	
tac ctg gag aca cgt ctg gct gac tgg atc cac agc agt ggc ggc tgg	432
Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gca cgg	480
Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg	
145 150 155 160	
cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg	528
Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly	
165 170 175	

gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576  
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
                   180                                  185                                  190

aag tga 582  
 Lys

<210> 9  
 <211> 193  
 <212> PRT  
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                   20                                  25                                  30  
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala  
                   35                                  40                                  45  
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu  
                   50                                  55                                  60  
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr  
                   65                                  70                                  75                                  80  
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu  
                                   85                                  90                                  95  
 Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn  
                   100                                  105                                  110  
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Met Val Ala  
                   115                                  120                                  125  
 Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp  
                   130                                  135                                  140  
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg  
                   145                                  150                                  155                                  160  
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly  
                                   165                                  170                                  175  
 Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser  
                   180                                  185                                  190  
 Lys